

09/674235

Sequence listing

<110> Sagami Chemical Research Center

5 <120> Human Proteins Having Transmembrane Domains and DNAs Encoding these Proteins

<130> 661099

10 <140>

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<150> JP 10-119395

<151> 1998-04-28

15 <160> 36

<170> Windows 95 (Word 98)

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<210> 1

<211> 268

<212> PRT

<213> Homo sapiens

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Gln Met Leu His Leu Val Phe Ile Leu Pro Ser Leu Met Leu Leu Ile

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20 25

30

Pro His Ile Leu Leu Glu Asn Phe Ala Ala Ala Ile Pro Gly His Arg

35 40 45

Cys Trp Val His Met Leu Asp Asn Asn Thr Gly Ser Gly Asn Glu Thr

50 55 60

35 Gly Ile Leu Ser Glu Asp Ala Leu Leu Arg Ile Ser Ile Pro Leu Asp

65 70 75 80
Ser Asn Leu Arg Pro Glu Lys Cys Arg Arg Phe Val His Pro Gln Trp
 85 90 95
Gln Leu Leu His Leu Asn Gly Thr Ile His Ser Thr Ser Glu Ala Asp
5 100 105 110
Thr Glu Pro Cys Val Asp Gly Trp Val Tyr Asp Gln Ser Tyr Phe Pro
 115 120 125
Ser Thr Ile Val Thr Lys Trp Asp Leu Val Cys Asp Tyr Gln Ser Leu
 130 135 140
10 Lys Ser Val Val Gln Phe Leu Leu Leu Thr Gly Met Leu Val Gly
 145 150 155 160
Ile Ile Gly Gly His Val Ser Asp Arg Trp Leu Val Glu Ser Ala Arg
 165 170 175
Trp Leu Ile Ile Thr Asn Lys Leu Asp Glu Gly Leu Lys Ala Leu Arg
15 180 185 190
Lys Val Ala Arg Thr Asn Gly Ile Lys Asn Ala Glu Glu Thr Leu Asn
 195 200 205
Ile Glu Val Val Arg Ser Thr Met Gln Glu Glu Leu Asp Ala Ala Gln
 210 215 220
20 Thr Lys Thr Thr Val Cys Asp Leu Phe Arg Asn Pro Ser Met Arg Lys
 225 230 235 240
Arg Ile Cys Ile Leu Val Phe Leu Arg Lys Lys Ile Ser Arg Lys Arg
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His Lys Asn Asp Cys Tyr Thr Lys Val Thr Lys Phe
25 260 265

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30 <213> Homo sapiens

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	35	40	45
	His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly Phe Val Phe		
5	50	55	60
	Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile		
	65	70	75
	Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser		
	85	90	95
10	Phe Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu		
	100	105	110
	Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser		
	115	120	125
	Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His Ile Asn Arg		
15	130	135	140
	Ala Leu Lys Leu Ile Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp		
	145	150	155
	Ser Leu Lys Leu Ala Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala		
	165	170	175
20	Val Phe Asn Gly Ile Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe		
	180	185	190
	Ser Val Pro Ile Val Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr		
	195	200	205
	Val Gly Ile Ala Arg Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln		
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	Ala Lys Leu Pro Gly Ile Ala Lys Lys Lys Ala Glu		
	225	230	235
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	<212> PRT		
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Tyr Val Ser Ile Leu Leu Gln Ser Asp Lys Lys Leu Thr Gln Glu Gln
5 35 40 45
Val Ser Asp Ser Gln Val Leu Ile Arg Ser Arg Val Leu Arg Glu Asn
50 55 60
Gly Lys Tyr Ile Pro Lys Gln Ser Phe Leu Thr Arg Lys Tyr Tyr Phe
65 70 75 80
10 Asn Asn Pro Glu Asp Gly Phe Phe Lys Lys Thr Lys Arg Lys Val Val
85 90 95
Pro Pro Ser Pro Met Thr Asp Pro Thr Met Leu Thr Asp Met Met Lys
100 105 110
Gly Asn Val Thr Asn Val Leu Pro Met Ile Leu Ile Gly Gly Trp Ile
15 115 120 125
Asn Met Thr Phe Ser Gly Phe Val Thr Thr Lys Val Pro Phe Pro Leu
130 135 140
Thr Leu Arg Phe Lys Pro Met Leu Gln Gln Gly Ile Glu Leu Leu Thr
145 150 155 160
20 Leu Asp Ala Ser Trp Val Ser Ser Ala Ser Trp Tyr Phe Leu Asn Val
165 170 175
Phe Gly Leu Arg Ser Ile Tyr Ser Leu Ile Leu Gly Gln Asp Asn Ala
180 185 190
Ala Asp Gln Ser Arg Met Met Gln Glu Gln Met Thr Gly Ala Ala Met
25 195 200 205
Ala Met Pro Ala Asp Thr Asn Lys Ala Phe Lys Thr Glu Trp Glu Ala
210 215 220
Leu Glu Leu Thr Asp His Gln Trp Ala Leu Asp Asp Val Glu Glu Glu
225 230 235 240
30 Leu Met Ala Lys Asp Leu His Phe Glu Gly Met Phe Lys Glu Leu
245 250 255
Gln Thr Ser Ile Phe
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<211> 328

<212> PRT

<213> Homo sapiens

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35 40 45

Gln Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val

50 55 60

Glu Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln

15 65 70 75 80
Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile

85 90 95

Leu Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys
100 105 11020 Leu Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe Phe Thr
115 120 125

Gly Arg Lys Arg Asn Val Glu His Trp Ile Gly His Glu Asn Phe Glu

130 135 140

Leu Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile Glu Gly Val Glu

25 145 150 155 160
Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly Pro Arg Met His Met

165 170 175

Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu Gln Ala Leu Gln Gly
180 185 19030 Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln Thr Arg Ala Phe Gln
195 200 205Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala Leu Met Asn Ser Asn
210 215 220

Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu Glu His Thr Ile Leu

35 225 230 235 240

Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly Ser Gly Ser Glu Ile
245 250 255
Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln Lys Arg Lys Pro Asp
260 265 270
Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu Pro Val Val Pro Leu
275 280 285
Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe Arg Lys Glu Leu Glu
290 295 300
Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro Lys Pro Ala Arg Ile
10 305 310 315 320
Lys Lys Gly Arg Thr Arg His Ser
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15 <211> 300
<212> PRT
<213> Homo sapiens

<400> 5
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Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
20 25 30
Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
25 35 40 45
Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
50 55 60
Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
65 70 75 80
30 Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
85 90 95
Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110
Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
35 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
130 135 140
Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
145 150 155 160
5 Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
165 170 175
Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
180 185 190
Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
10 195 200 205
Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
210 215 220
Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225 230 235 240
15 Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
245 250 255
Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
260 265 270
Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
20 275 280 285
Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 6
25 <211> 182
<212> PRT
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Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
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Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
35 35 40 45

Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
50 55 60
Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
65 70 75 80
5 Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
85 90 95
Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
100 105 110
Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
10 115 120 125
Ile Ser Gly Thr Leu Lys Phe Ala Cys Glu Ser Ile Val Glu Glu Tyr
130 135 140
Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
145 150 155 160
15 Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
165 170 175
Ile Ser His Asp Glu Leu
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20 <210> 7
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<213> Homo sapiens

25 <400> 7
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Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn Phe Asp Val Arg Pro
20 25 30
30 Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser Tyr Trp Leu Asp Leu
35 40 45
Trp Leu Phe Ile Leu Phe Asp Val Val Phe Leu Phe Val Tyr Phe
50 55 60
Leu Pro
35 65

<210> 8

<211> 183

<212> PRT

5 <213> Homo sapiens

<400> 8

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10 Phe Gln His Arg Glu Arg Val Ala Met His Tyr Gln Met Ser Val Thr
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Leu Lys Tyr Glu Ile Lys Lys Leu Ile Tyr Val His Leu Val Ile Trp

35 40 45

15 Leu Leu Leu Val Ala Lys Met Ser Val Gly His Leu Arg Leu Leu Ser
50 55 60

His Asp Gln Val Ala Met Pro Tyr Gln Trp Glu Tyr Pro Tyr Leu Leu

65 70 75 80

Ser Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser Phe Pro Arg Asn Asn
85 90 95

20 Ile Ser Tyr Leu Val Leu Ser Met Ile Ser Met Gly Leu Phe Ser Ile
100 105 110

Ala Pro Leu Ile Tyr Gly Ser Met Glu Met Phe Pro Ala Ala Gln Gln
115 120 125

Leu Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu Phe Gly Phe Ser Ala

25 130 135 140

Val Ser Ile Met Tyr Leu Val Leu Val Ala Val Gln Val His Ala

145 150 155 160

Trp Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp Ser Trp Phe Thr Ser
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30 Thr Gln Glu Lys Lys His Lys

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<210> 9

<211> 324

35 <212> PRT

<213> Homo sapiens

<400> 9

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Ala Leu Val Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro
35 40 45
10 Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser
50 55 60
Arg Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe
65 70 75 80
Leu Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile
15 85 90 95
Asp Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln
100 105 110
Glu Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln
115 120 125
20 Ile Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu
130 135 140
Thr Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His
145 150 155 160
Asp Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser
25 165 170 175
Ala Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val
180 185 190
Phe Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met
195 200 205
30 Glu Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser
210 215 220
Leu Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala
225 230 235 240
Gly Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu
35 245 250 255

Gly Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln

260

265

270

Ser Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe

275

280

285

5 Leu Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu

290

295

300

Lys Val Ile Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu

305

310

315

320

Phe Ile Gln Ile

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<210> 10

<211> 804

<212> DNA

<213> Homo sapiens

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<400> 10

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gctgcagcca ttccctggta tcgttgctgg gtccacatgc tggacaataa tactggatct 180

20

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tcaaattctga ggccagagaa gtgtcgtcgc tttgtccatc cccagtggca gtttcttcac 300

ctgaatggaa ctatccacag cacaagttag gcagacacag aaccctgtgt ggtatggctgg 360

gtatatgatc aaagctactt cccttcgacc attgtgacta agtggaccc ggtatgtat 420

tatcagtcac tgaaatcagt ggttcaattc ctacttctga ctggaatgct ggtggaggc 480

25

atcataggtg gccatgtctc agacaggtgg ctgggtgaat ctgtcggtg gttgataatc 540

accaataaaac tagatgaggg cttaaaggca cttagaaaaag ttgcacgcac aaatggaata 600

aagaatgtg aagaaaccctt gaacatagag gttgttaagat ccaccatgca ggaggagctg 660

gatgcagcac agacaaaaac tactgtgtgt gacttggatcc gcaacccca gatgcgtaaa 720

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<210> 11

<211> 708

<212> DNA

35 <213> Homo sapiens

<400> 11

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5	agctgcagct	cctccgtgtc	ggtgcacgat	ctgattttct	ggagayatgt	gaagaagact	180
	gggtttgtct	ttggcaccac	gctgatcatg	ctgcttccc	tggcagctt	cagtgtcatc	240
	agtgtggttt	cttacctcat	cctggctctt	ctctctgtca	ccatcagctt	caggatctac	300
	aagtccgtca	tccaagctgt	acagaagtca	gaagaaggcc	atccattcaa	agcctacctg	360
	gacgttagaca	ttactctgtc	ctcagaagct	ttccataatt	acatgaatgc	tgccatggtg	420
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	tacaagaccc	agattgatca	ctatgttggc	atgcggcag	atcagaccaa	gtcaattgtt	660
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<211> 783

<212> DNA

<213> Homo sapiens

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<400> 12

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	gacaagaagc	tcacccagga	acaagtatct	gacagtcaag	tcctaattcg	aagcagagtc	180
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	atgactgatc	ctactatgtt	gacagacatg	atgaaaggga	atgtaacaaa	tgcctccct	360
	atgattctta	ttggtgatg	gatcaacatg	acatttcag	gctttgtcac	aaccaaggtc	420
	ccatattccac	tgaccctccg	tttaagcct	atgttacagc	aaggaatoga	gctactcaca	480
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	gagcagatga	cgggagcagc	catggccatg	cccgccagaca	caaacaagc	tttcaagaca	660
	gagtggaaag	ctttggagct	gacggatcac	cagtggcac	tagatgatgt	cgaagaagag	720
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<211> 984

<212> DNA

5 <213> Homo sapiens

<400> 13

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10 agctttctac tcaacaggta tatccagaa aatggtaac taaaaattga aagcaagatt 180

gaagagatgg ttgaaccact aagagagaaa atcagagatt tagaaaaaaag cttaaccag 240

aaataccac cagtaaagtt tttatcagaa aaggatcggaa aagaatttt gataacagga 300

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accgtggtgg acaatttctt cacggcagg aagagaaaacg tggagcactg gatcgacat 420

15 gagaacttcg agttgattaa ccacgacgtg gtggagcccc tctacatcga gggcgtggaa 480

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gtagtcagca acttcatcct gcaggcgctc cagggggagc cactcacggt atacggatcc 600

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atgaacagca acgtcagcag cccggtaaac ctggggaaacc cagaagaaca cacaatccta 720

20 gaatttgctc agttaattaa aaaccttgtt gtagcgaa gtagaaattca gtttctctcc 780

gaagcccagg atgaccaca gaaaagaaaa ccagacatca aaaaagcaaa gctgatgctg 840

gggtgggagc ccgtgtccc gctggaggaa gtttaaaca aagcaattca ctactccgt 900

aaagaactcg agtaccaggc aaataatcag tacatccccaa accaaagcc tgccagaata 960

aagaaaggac ggactcgcca cagc 984

25

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<212> DNA

<213> Homo sapiens

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<400> 14

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attacaggag ctgggcatgg aattgggaga ctgactgcct atgaaatttc taaaacttaaa 180

35 agcaagctgg ttctctggaa tataaataag catggactgg aggaaacagc tgccaaatgc 240

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gctggtag t_{catac}atc agatttgtt gctacacaag atcctcagat tgaaaagact 420
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5 aagaataacc atggccat_{at} t_{gtcact}gtg g_{ttcg}gcag ctggacatgt ctgggtcccc 540
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gatgaactgg ctgc_cttaca aataactgga gtcaaaacaa catgtctgtg tcctaattc 660
gt_{aa}acactg g_{tt}catcaa aaatcca_{ag}t acaagttgg gacccactct ggaacctgag 720
gaagtggtaa acaggctgat gcatggatt ctgactgagc agaagatgat ttttattcca 780
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<210> 15

<211> 546

15 <212> DNA

<213> Homo sapiens

<400> 15

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gaaattgccc aggtggaccc caagaagacc attcagatgg gatcttccg gatcaatcca 180
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catcgcaaga actacgtacg t_{gt}atgtggc_{gc} c_ggaatggag aatcc_{at}gtga actggaccta 360
25 caaggcatcc gaatcgactc agatatt_{at}gc ggcaccc_{tc}a agtttgc_{gt}tg tgagagcatt 420
gtggaggaat acgaggatga actcattgaa ttctttccc gagaggctga caatgtaaa 480
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gagcta

30 <210> 16

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<212> DNA

<213> Homo sapiens

35 <400> 16

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	tgtgtactgg tttctccct ggcctccac tccgtttcg aggggctggc ggttagggctg		600
	cagcgagacc gggctcgggc catggagctg tgcctggctt tgctgctcca caagggcatc		660
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	gcagagtcgg caggaccttgc accagctg gcccagtctg tgctagaggg catggcagct		840
	ggcacccccc tctatatcac ctttctggaa atcctgcccc aggagctggc cagttctgag		900
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	Glu Thr Gly Ile Leu Ser Glu Asp Ala Leu Leu Arg Ile Ser Ile Pro		
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19.

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	Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro Lys Pro Ala Arg Ile			
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	aag aaa gga cgg act cgc cac agc tgaactcctc acttttagga cacaagac			1070
	Lys Lys Gly Arg Thr Arg His Ser			
25	325			
	taccattgt a cacttgatgg gatgtat tttt tggcttttt ttgttgtcgt ttaaagaaag			1130
	actttaacag gtgtcatgaa gaacaaactg gaatttcatt ctgaagcttgc tttaatgaa			1190
	atggatgtgc ctaaaagctc ccctcaaaaa actgcagatt ttgccttgca cttttgaat			1250
	ctctctttt atgtaaaata gcgttagatgc atctctgcgt atttcaagt ttttttatct			1310
30	tgctgtgaga gcatatgtt tgactgtcgt tgacagttt atttactggt ttctttgtga			1370
	agctgaaaag gaacattaag cgggacaaaa aatgccgatt ttatataa aagtgggtac			1430
	ttaataaatg agtcgttata ctatgcataa agaaaaatcc tagcagtatt gtcaggtgg			1490
	ggtgcggccgg cattgat tttt agggcagata aaagaattct gtgtgagagc tttatgttc			1550
	tcttttaatt cagagttttt ccaaggctca ctttgagtt gcaaacttga ctggaaata			1610
35	ttcctgttgg tcatgatcaa ggatattga aatcaactact gtgtttgct gcttatctgg			1670

ggcggggca gggtggggg cacaaggta acatattctt ggttaaccat ggttaaatat 1730
gctattttaa taaaatattg aaactcacc 1759

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5 <211> 328

<212> PRT

<213> Homo sapiens

<400> 26

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1 5 10 15
Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
20 25 30
Val Trp Gly Asn Phe Val Asn Met Ser Phe Leu Leu Asn Arg Ser Ile
15 35 40 45
Gln Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val
50 55 60
Glu Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln
65 70 75 80
20 Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile
85 90 95
Leu Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys
100 105 110
Leu Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe Phe Thr
25 115 120 125
Gly Arg Lys Arg Asn Val Glu His Trp Ile Gly His Glu Asn Phe Glu
130 135 140
Leu Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile Glu Gly Val Glu
145 150 155 160
30 Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly Pro Arg Met His Met
165 170 175
Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu Gln Ala Leu Gln Gly
180 185 190
Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln Thr Arg Ala Phe Gln
35 195 200 205

Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala Leu Met Asn Ser Asn
 210 215 220
 Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu Glu His Thr Ile Leu
 225 230 235 240
 5 Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly Ser Gly Ser Glu Ile
 245 250 255
 Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln Lys Arg Lys Pro Asp
 260 265 270
 Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu Pro Val Val Pro Leu
 10 275 280 285
 Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe Arg Lys Glu Leu Glu
 290 295 300
 Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro Lys Pro Ala Arg Ile
 305 310 315 320
 15 Lys Lys Gly Arg Thr Arg His Ser
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 <211> 1697
 20 <212> DNA
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 ccacaaaagg g atg aaa ttt ctt ctg gac atc ctc ctg ctt ctc ccg tta 170
 Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu
 1 5 10
 ctg atc gtc tgc tcc cta gag tcc ttc gtg aag ctt ttt att cct aag 218
 30 Leu Ile Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys
 15 20 25
 agg aga aaa tca gtc acc ggc gaa atc gtg ctg att aca gga gct ggg 266
 Arg Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
 30 35 40 45
 35 cat gga att ggg aga ctg act gcc tat gaa ttt gct aaa ctt aaa agc 314

	His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser			
	50	55	60	
	aag ctg gtt ctc tgg gat ata aat aag cat gga ctg gag gaa aca gct		362	
	Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala			
5	65	70	75	
	gcc aaa tgc aag gga ctg ggt gcc aag gtt cat acc ttt gtg gta gac		410	
	Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp			
	80	85	90	
	tgc agc aac cga gaa gat att tac agc tct gca aag aag gtg aag gca		458	
10	Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala			
	95	100	105	
	gaa att gga gat gtt agt att tta gta aat aat gct ggt gta gtc tat		506	
	Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr			
	110	115	120	125
15	aca tca gat ttg ttt gct aca caa gat cct cag att gaa aag act ttt		554	
	Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe			
	130	135	140	
	gaa gtt aat gta ctt gca cat ttc tgg act aca aag gca ttt ctt cct		602	
	Glu Val Asn Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro			
20	145	150	155	
	gca atg acg aag aat aac cat ggc cat att gtc act gtg gct tcg gca		650	
	Ala Met Thr Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala			
	160	165	170	
	gct gga cat gtc tcg gtc ccc ttc tta ctg gct tac tgt tca agc aag		698	
25	Ala Gly His Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys			
	175	180	185	
	ttt gct gct gtt gga ttt cat aaa act ttg aca gat gaa ctg gct gcc		746	
	Phe Ala Ala Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala			
	190	195	200	205
30	tta caa ata act gga gtc aaa aca aca tgt ctg tgt cct aat ttc gta		794	
	Leu Gln Ile Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val			
	210	215	220	
	aac act ggc ttc atc aaa aat cca agt aca agt ttg gga ccc act ctg		842	
	Asn Thr Gly Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu			
35	225	230	235	

gaa cct gag gaa gtg gta aac agg ctg atg cat ggg att ctg act gag 890
 Glu Pro Glu Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu
 240 245 250
 cag aag atg att ttt att cca tct tct ata gct ttt tta aca aca ttg 938
 5 Gln Lys Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu
 255 260 265
 gaa agg atc ctt cct gag cgt ttc ctg gca gtt tta aaa cga aaa atc 986
 Glu Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
 270 275 280 285
 10 agt gtt aag ttt gat gca gtt att gga tat aaa atg aaa gcg caa 1031
 Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300
 taaggacct agttttctga aaactgattt accagggtta ggttcatgtc atctaataatgt 1090
 gccagaattt taatgtttga acttctgttt tttctaatta tccccatttc ttcaatatca 1150
 15 ttttgaggc tttggcagtc ttcattttact accacttggtt ctttagccaa aagctgatta 1210
 catatgatat aaacagagaa ataccttag aggtgacttt aaggaaaaatg aagaaaaaaga 1270
 accaaaaatga ctttattaaa ataatttcca agattatttg tggctcacct gaaggcttg 1330
 caaaaattgt accataaccg tttatTTAAC atatattttt atttttgatt gcacttaaat 1390
 tttgtataat ttgtgtttct tttctgttc tacataaaaat cagaaacttc aagctctcta 1450
 20 aataaaaatga aggactatat ctatgtgtat ttcacaatga atatcatgaa ctctcaatgg 1510
 gtaggtttca tcctacccat tgccactctg tttcctgaga gatacctcac attccaatgc 1570
 caaacatttc tgcacaggga agctagaggt ggatacacgt gttgcaagta taaaagcatc 1630
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 25 <210> 28
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 <213> Homo sapiens
 30 <400> 28
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 Leu Ile Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys
 35 15 20 25

Arg Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
30 35 40 45
His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser
50 55 60
Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala
65 70 75
Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp
80 85 90
Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala
10 95 100 105
Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr
110 115 120 125
Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe
130 135 140
15 Glu Val Asn Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro
145 150 155
Ala Met Thr Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala
160 165 170
Ala Gly His Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys
20 175 180 185
Phe Ala Ala Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala
190 195 200 205
Leu Gln Ile Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val
210 215 220
25 Asn Thr Gly Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu
225 230 235
Glu Pro Glu Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu
240 245 250
Gln Lys Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu
30 255 260 265
Glu Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
270 275 280 285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

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<211> 814
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<213> *Homo sapiens*

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 aagttagat ccagcggtct tccagcgctt gggccacggc ggccggccctg ggagcagagg 120
 tggagcgacc ccattacgct aaag atg aaa ggc tgg ggt tgg ctg gcc ctg 171
 10 Met Lys Gly Trp Gly Trp Leu Ala Leu
 1 5
 ctt ctg ggg gcc ctg gga acc gcc tgg gct cgg agg agc cag gat 219
 Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
 10 15 20 25
 15 ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa 267
 Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
 30 35 40
 att gcc cag gtg gac ccc aag aag acc att cag atg gga tct ttc cgg 315
 Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
 20 45 50 55
 atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat gcc cgc 363
 Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr Ala Arg
 60 65 70
 tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac cgg atg 411
 Ser Glu Ala His Leu Thr Glu Leu Leu Glu Ile Cys Asp Arg Met
 25 75 80 85
 aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag aac tac 459
 Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys Asn Tyr
 90 95 100 105
 30 gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac cta caa 507
 Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp Leu Gln
 110 115 120
 ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt gcg tgt 555
 Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe Ala Cys
 35 125 130 135

	gag agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc ttt tcc	603
	Glu Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe Phe Ser	
	140 145 150	
	cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga aca gat	651
5	Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg Thr Asp	
	155 160 165	
	ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta tgaaccactg	700
	Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu	
	170 175 180	
10	gagcagccca cactggcttg atggatcacc cccaggaggg gaaaaatggtg gcaatgcctt	760
	ttatatatta tgttttact gaaattaact gaaaaaatat gaaaccaaaa gtac	814

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	<211> 182			
15	<212> PRT			
	<213> Homo sapiens			
	 <400> 30			
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20		1	5	
	Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp			
	10 15 20 25			
	Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu			
	30 35 40			
25	Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg			
	45 50 55			
	Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr Ala Arg			
	60 65 70			
	Ser Glu Ala His Leu Thr Glu Leu Leu Glu Ile Cys Asp Arg Met			
30	75 80 85			
	Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys Asn Tyr			
	90 95 100 105			
	Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp Leu Gln			
	110 115 120			
35	Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe Ala Cys			

DRAFT-0992960

	125	130	135	
	Glu Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe Phe Ser			
	140	145	150	
	Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg Thr Asp			
5	155	160	165	
	Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu			
	170	175	180	
	<210> 31			
10	<211> 511			
	<212> DNA			
	<213> Homo sapiens			
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	Met Glu Val Asp Ala Pro Gly Val Asp Gly			
	1	5	10	
	CGA GAT GGT CTC CGG GAG CGG CGA GGC TTT AGC GAG GGA GGG AGG CAG			100
	Arg Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln			
20	15	20	25	
	aac ttc gat gtc agg cct cag tct ggg gca aat ggg ctt ccc aaa cac			148
	Asn Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His			
	30	35	40	
	tcc tac tgg ttg gac ctc tgg ctt ttc atc ctt ttc gat gtc gtc gtc			196
25	Ser Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val			
	45	50	55	
	ttt ctc ttt gtc tat ttt ttg cca tgacttgttc gctgatatct aaattaagaa			250
	Phe Leu Phe Val Tyr Phe Leu Pro			
	60	65		
30	gttggttctt gagtgaattc tgaaaaatggc tacaaacttc ttgaataaaag aagacaggac			310
	tctcaataga agaatttcac atctccaagg gacccttctt ttcattttac actttgttac			370
	taattttgcag aactctatta attgggttagg atttcaccca ttccctagcta agttcttaaa			430
	attaaaccct ttgggtcggt tttaaaaact ttcaaacatc tggatggctt acaggggctg			490
	aatataaaag catttgtact t			511

<210> 32
<211> 66
<212> PRT
<213> Homo sapiens

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<400> 32

Met Glu Val Asp Ala Pro Gly Val Asp Gly
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Arg Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln

10

15 20 25

Asn Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His

30 35 40

Ser Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val

45 50 55

15

Phe Leu Phe Val Tyr Phe Leu Pro

60 65

<210> 33

<211> 1126

20

<212> DNA

<213> Homo sapiens

<400> 33

ctcttcacgg agccgcgcgg ctgcgggggc gcaaataggg tcactgggcc gcttggcggt 60

25 gtcgttgcgg taccagggtcc gcgtgaggggg ttccgggggtt ctgggcaggc aca atg 116
Met

1

gcg tct cga gca ggc ccg cga gcg gcc ggc acc gac ggc agc gac ttt 164
Ala Ser Arg Ala Gly Pro Arg Ala Ala Gly Thr Asp Gly Ser Asp Phe

30

5 10 15

cag cac ccg gag cgc gtc gcc atg cac tac cag atg agt gtg acc ctc 212
Gln His Arg Glu Arg Val Ala Met His Tyr Gln Met Ser Val Thr Leu

20 25 30

35 aag tat gaa atc aag aag ctg atc tac gta cat ctg gtc ata tgg ctg 260
Lys Tyr Glu Ile Lys Lys Leu Ile Tyr Val His Leu Val Ile Trp Leu

	35	40	45	
	ctg ctg gtt gct aag atg agc gtg gga cac ctg agg ctc ttg tca cat			308
	Leu Leu Val Ala Lys Met Ser Val Gly His Leu Arg Leu Leu Ser His			
	50	55	60	65
5	gat cag gtg gcc atg ccc tat cag tgg gaa tac ccg tat ttg ctg agc			356
	Asp Gln Val Ala Met Pro Tyr Gln Trp Glu Tyr Pro Tyr Leu Leu Ser			
	70	75	80	
	att ttg ccc tct ctc ttg ggc ctt ctc tcc ttt ccc cgc aac aac att			404
	Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser Phe Pro Arg Asn Asn Ile			
10	85	90	95	
	agc tac ctg gtg ctc tcc atg atc agc atg gga ctc ttt tcc atc gct			452
	Ser Tyr Leu Val Leu Ser Met Ile Ser Met Gly Leu Phe Ser Ile Ala			
	100	105	110	
	cca ctc att tat ggc agc atg gag atg ttc cct gct gca cag cag ctc			500
15	Pro Leu Ile Tyr Gly Ser Met Glu Met Phe Pro Ala Ala Gln Gln Leu			
	115	120	125	
	tac cgc cat ggc aag gcc tac cgt ttc ctc ttt ggt ttt tct gcc gtt			548
	Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu Phe Gly Phe Ser Ala Val			
	130	135	140	145
20	tcc atc atg tac ctg gtg ttg gtg ttg gca gtg caa gtg cat gcc tgg			596
	Ser Ile Met Tyr Leu Val Leu Val Leu Ala Val Gln Val His Ala Trp			
	150	155	160	
	cag ttg tac tac agc aag aag ctc cta gac tct tgg ttc acc agc aca			644
	Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp Ser Trp Phe Thr Ser Thr			
25	165	170	175	
	cag gag aag aag cat aaa tgaaggctct ttggggtgaa gcctggacat cccatcgaa			700
	Gln Glu Lys Lys His Lys			
	180			
	atgaaaaggac actagtacag cggttccaaa atcccttctg gtgatttttag cagctgtgat			760
30	gttggtacct ggtgcagacc aggccaaagt tctgaaagc tcctttgcc atctgctgag			820
	gtggccaaac tataatttat tcctggttgg ctagaactgg gtgaccgaca gctatgaaac			880
	aaatttcagc tgtttgaagt tgaactttga ggaaaaatggat taagaatgag ctccgtccctt			940
	gcctctactc ggtcattctc cccatttcca tccattaccc cttagccatt gagactaaag			1000
	gaaataggaa ataaatcaa ttacttcatc tctaggtcac gggtcagggaa acatttgggc			1060
35	agctgctccc ttggcagctg tggctccctc tgcaaagcat tttaaattaaa aacctaata			1120

aagatg

1126

<210> 34

<211> 183

5 <212> PRT

<213> Homo sapiens

<400> 34

Met

10

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 5 10 15

Gln His Arg Glu Arg Val Ala Met His Tyr Gln Met Ser Val Thr Leu
 20 25 30

15

Lys Tyr Glu Ile Lys Lys Leu Ile Tyr Val His Leu Val Ile Trp Leu
 35 40 45

Leu Leu Val Ala Lys Met Ser Val Gly His Leu Arg Leu Leu Ser His
 50 55 60 65

Asp Gln Val Ala Met Pro Tyr Gln Trp Glu Tyr Pro Tyr Leu Leu Ser
 70 75 80

20

Ile Leu Pro Ser Leu Leu Gly Leu Leu Ser Phe Pro Arg Asn Asn Ile
 85 90 95

Ser Tyr Leu Val Leu Ser Met Ile Ser Met Gly Leu Phe Ser Ile Ala
 100 105 110

25

Pro Leu Ile Tyr Gly Ser Met Glu Met Phe Pro Ala Ala Gln Gln Leu
 115 120 125

Tyr Arg His Gly Lys Ala Tyr Arg Phe Leu Phe Gly Phe Ser Ala Val
 130 135 140 145

30

Ser Ile Met Tyr Leu Val Leu Val Leu Ala Val Gln Val His Ala Trp
 150 155 160

Gln Leu Tyr Tyr Ser Lys Lys Leu Leu Asp Ser Trp Phe Thr Ser Thr
 165 170 175

Gln Glu Lys Lys His Lys

180

<210> 35
<211> 2015
<212> DNA
<213> *Homo sapiens*

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 Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala Val
 5 10 15
 gct tca gag cct cca gtg cct gtg ggg ctg gag gtg aag ttg ggg gcc 152
 Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly Ala
 15 20 25 30
 ctg gtg ctg ctg ctg gtg ctc acc ctc ctc tgc agc ctg gtg ccc atc 200
 Leu Val Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro Ile
 35 40 45
 tgt gtg ctg cgc cgg cca gga gct aac cat gaa ggc tca gct tcc cgc 248
 Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser Arg
 20 50 55 60 65
 cag aaa gcc ctg agc cta gta agc tgt ttc gcg ggg ggc gtc ttt ttg 296
 Gln Lys Ala Leu Ser Leu Val Ser Cys Phe Ala Gly Gly Val Phe Leu
 70 75 80
 25 gcc act tgt ctc ctg gac ctg ctg cct gac tac ctg gct gcc ata gat 344
 Ala Thr Cys Leu Leu Asp Leu Leu Pro Asp Tyr Leu Ala Ala Ile Asp
 85 90 95
 gag gcc ctg gca gcc ttg cac gtg acg ctc cag ttc cca ctg caa gag 392
 Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
 30 100 105 110
 ttc atc ctg gcc atg ggc ttc ttc ctg gtc ctg gtg atg gag cag atc 440
 Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
 115 120 125
 aca ctg gct tac aag gag cag tca ggg ccg tca cct ctg gag gaa aca 488
 Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
 35

130	135	140	145	
agg gct ctg ctg gga aca gtg aat ggt ggg ccg cag cat tgg cat gat Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His Asp				536
150	155	160		
ggg cca ggg gtc cca cag gcg agt gga gcc cca gca acc ccc tca gcc Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala				584
165	170	175		
ttg cgt gcc tgt gta ctg gtg ttc tcc ctg gcc ctc cac tcc gtg ttc Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe				632
180	185	190		
gag ggg ctg gcg gta ggg ctg cag cga gac cgg gct cgg gcc atg gag Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu				680
195	200	205		
ctg tgc ctg gct ttg ctg ctc cac aag ggc atc ctg gct gtc agc ctg Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu				728
210	215	220	225	
tcc ctg cgg ctg ttg cag agc cac ctt agg gca cag gtg gtg gct ggc Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala Gly				776
230	235	240		
tgt ggg atc ctc ttc tca tgc atg aca cct cta ggc atc ggg ctg ggt Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly				824
245	250	255		
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260	265	270		
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275	280	285		
gaa atc ctg ccc cag gag ctg gcc agt tct gag caa agg atc ctc aag Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys				968
290	295	300	305	
gtc att ctg ctc cta gca ggc ttt gcc ctg ctc act ggc ctg ctc ttc Val Ile Leu Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu Phe				1016
310	315	320		
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The Gln IIe

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<212> PRT
<213> *Homo sapiens*

25 <400> 36

Met

1

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5 Glu Ala Leu Ala Ala Leu His Val Thr Leu Gln Phe Pro Leu Gln Glu
100 105 110
Phe Ile Leu Ala Met Gly Phe Phe Leu Val Leu Val Met Glu Gln Ile
115 120 125
Thr Leu Ala Tyr Lys Glu Gln Ser Gly Pro Ser Pro Leu Glu Glu Thr
10 130 135 140 145
Arg Ala Leu Leu Gly Thr Val Asn Gly Gly Pro Gln His Trp His Asp
150 155 160
Gly Pro Gly Val Pro Gln Ala Ser Gly Ala Pro Ala Thr Pro Ser Ala
165 170 175
15 Leu Arg Ala Cys Val Leu Val Phe Ser Leu Ala Leu His Ser Val Phe
180 185 190
Glu Gly Leu Ala Val Gly Leu Gln Arg Asp Arg Ala Arg Ala Met Glu
195 200 205
Leu Cys Leu Ala Leu Leu Leu His Lys Gly Ile Leu Ala Val Ser Leu
20 210 215 220 225
Ser Leu Arg Leu Leu Gln Ser His Leu Arg Ala Gln Val Val Ala Gly
230 235 240
Cys Gly Ile Leu Phe Ser Cys Met Thr Pro Leu Gly Ile Gly Leu Gly
245 250 255
25 Ala Ala Leu Ala Glu Ser Ala Gly Pro Leu His Gln Leu Ala Gln Ser
260 265 270
Val Leu Glu Gly Met Ala Ala Gly Thr Phe Leu Tyr Ile Thr Phe Leu
275 280 285
Glu Ile Leu Pro Gln Glu Leu Ala Ser Ser Glu Gln Arg Ile Leu Lys
30 290 295 300 305
Val Ile Leu Leu Leu Ala Gly Phe Ala Leu Leu Thr Gly Leu Leu Phe
310 315 320
Ile Gln Ile